

SEQUENCE LISTINGS

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(B) TISSUE TYPE: Dorsal root ganglion

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 292..1909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

spasic Length: 2622

1 AGTGACAGCT GTGCGGGTGC TGATAAGGGA AGCCACAAGG AGACGATCGA

51 GGAGAGAGAC AAGCGGCAGC AGAGGCAGCA GCGACAGATG CAGCGCCGGG

101 GCTGCGGAGC TGCTGGGAGT GGGAGTGACG CCCCCACCTC GGGCCCCCAC

151 CCTGTCCCCA TCCTCCTCCT GGTGCCCCTG AGTTTAGAAG AGCAGCCGCT

201 GCCACCACCA CCACTCCGGA GGGCACCAGG GCTGCTGTCC AGGGAAGGAC

251 AGTAGCAGTG AGGCTCTGGC CAGTCCCAGC AGCCGGGGAC AGATGCCGAT

301 CGAGATTGTG TGCAAAATCA AATTTGCTGA GGAGGATGCA AAACCCAAGG

351 AGAAGGAGGC AGGGGATGAG CAGAGCCTCC TGGGGGCTGC TCAGGGGCCA

401 GCAGCCCCCTC GGGACCTGGC TACCTTTGCC AGCACCAGTA CTCTGCATGG

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451 GCTGGGCCGG GCCTGTGGCC CAGGCCCCCA TGGACTGCGC AGAACCTGT
501 GGGTACTGGC CCTACTCACC TCACTGGCTG CCTTCCTGTA CCAGGCAGCC
551 AGCCTGGCCA GGGGCTACCT GACCCGGCCT CACCTGGTAG CCATGGACCC
601 TGCTGCCCCA GCCCCAGTGG CGGGCTTTCC GGCTGTCACC CTCTGCAACA
651 TCAACCGCTT CCGGCATTCT GCACTCAGCG ATGCTGATAT CTTCCACCTG
701 GCCAATCTGA CAGGGCTGCC CCCCAGAGAC CGGGATGGGC ACCGTGCAGC
751 TGGCCTTCGC TACCCAGAGC CTGACATGGT AGACATCCTC AACCGCAGT
801 GCCACCAGCT TGCTGACATG CTCAAGAGCT GCAACTTCAG TGGGCACCAC
851 TGCTCCGCCA GCAACTTCTC TGTGGTCTAT ACTCGCTATG GAAAGTGTTA
901 CACCTTCAAT GCAGATCCTC AGAGTTCACT GCCCAGCAGG GCAGGCGGCA
951 TGGGTAGTGG CCTGGAGATC ATGCTAGACA TCCAGCAGGA GGAATACCTA
1001 CCCATATGGA GGGAGACAAA TGAGACATCA TTCGAGGCAG GGATCCGGGT
1051 GCAGATCCAC AGCCAGGAGG AGCCTCCCTA CATCCACCAG CTGGGGTTCG
1101 GTGTGTCCCC AGGCTTCCAG ACTTTTGTGT CCTGCCAGGA ACAGCGGCTA
1151 ACTTATCTGC CCCAGCCTTG GGGCAACTGC CGGGCGGAAA GCAAGCTCAG
1201 GGAGCCTGAG CTTCAGGGCT ACTCAGCCTA TAGTGTGTCT GCCTGCCGAC
1251 TGCGCTGTGA GAAGGAGGCC GTGCTTCAGC GCTGCCACTG CCGGATGGTG
1301 CACATGCCAG GCAATGAGAC CATCTGCCCG CCAAATATCT ACATTGAATG
1351 TGCCGACCAC AACTGGACT CCCTGGGTGG GGGCTCTGAG GCGCCATGCT

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1401 TCTGCCCTAC ACCCTGCAAC CTGACTCGTT ACGGCAAAGA GATCTCCATG
1451 GTCAAGATCC CCAACAGGGG CTCTGCCAGG TACCTGGCGA GGAAGTACAA
1501 CCGCAATGAG ACCTACATAA GGGAAACTT CTTGGTCCTG GATGTCTTCT
1551 TTGAGGCCCT AACCTCTGAA GCCATGGAAC AGCGAGCTGC CTATGGTCTG
1601 TCAGCCTTGC TGGGGGACCT TGGGGGACAG ATGGGCCTGT TCATTGGGGC
1651 TAGCATCCTC ACCTTGCTGG AGATCCTTGA CTACATCTAT GAGGTCTCCT
1701 GGGATCGACT CAGAGGGTG TGGCGACGGC CCAAGACCCC ACTTAGGACG
1751 TCCACTGGGG GCATCTCCAC TTTGGGGCTG CAGGAAGTGA AGGAACAGAG
1801 TCCCTGTCCA AATCGAGGCC GTGCTGAGGG TGGTGGGGCT AGCAACCTGC
1851 TTCCCAACCA TCACCACCCC CACGGCCCCC CAGGAAGCCT CTTTGAAAAC
1901 TTTGCTTGCT AGGATGGTGC TGTGTGGGGA AAGTACCCAT GAAACCCAC
1951 ACTCTCCTAT TCCTGGGACA GAAGGTCTGG GGCAGCCCAG GGCTAAGGGA
2001 AGGGGTGGTG CTCCTGAAA GGCCAGGACT AGGGTCCTGC TCTCCCTGAC
2051 CTAGGCTCAG CTGCCTTGCA CAAGAATCCT TCTTGTCCAT ACTCCCTGCT
2101 CCCAGGCAGG TGTCCAGGAA GGGCTAGAGA CCGGACTANG AGGCCCCTGA
2151 GGAGGGGAGG GATGAAGAGA GGGAGGAAGG CGGAACCATG GTAGAGCCCC
2201 TCNGTACATT TGTATATATT TAGGGACTGG GTGGGGGTGG GACACAGACA
2251 TANAAGTTT GGGCTGCAGG GGAGGGTGAC ACAGGATAGT CAGGGTCCCA
2301 ACCCTAATGG CANAANGCAA CTCCTTGGGA CCTAGGCATG TTGGGCTGGT

2351 TCTACTTCCC TCTTTCCAGG CCCAGCTCCC TCTTGGCATG GGGAGTGGGT
2401 GGCCCATCAG GCCTGGCCCA GCTCCCANTT CCCCCTGTAC CAGCCCCACC
2451 ACAAGTTCCT TTCGTGGGGA GTGGGTGGAA ANACCTTTCA GACCTTGGCT
2501 AAGCTTATGG GGAGANGGAG TGGCCTTCTC ANGCTTGCT CCCTANAGAC
2551 TGGTTTTATA AANTGCTGGT GAACTTGGGA ATCNAGAGAC CCCNAGAAAA
2601 AAAAAAAAAA AAAAAAAAAA AA

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SPASIC protein

1 MPIEIVCKIK FAEEDAKPKE KEAGDEQSLL GAAQGPAAPR DLATFASTST
51 LHGLGRACGP GPHGLRRTLW VLALITSLAA FLYQAASLAR GYLTRPHLVA
101 MDPAAPAPVA GPPAVTLCNI NRFRHSALSD ADIFHLANLT GLPPKDRDGH
151 RAAGLRYPEP DMVDILNRTG HQLADMLKSC NFSGHHCSAS NFSVVYTRYG
201 KCYTFNADPQ SSLPSRAGGM GSGLEIMLDI QQEYLPPIWR ETNETSFEAG
251 IRVQIHSQEE PPYIHLGFG VSPGFQTFVS CQEQLTYLP QPWGNCRAES
301 KLREPELQGY SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPPNIY

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351 IECADHTLDS LGGGSEGPCF CPTPCNLTRY GKEISMVKIP NRGSAARYLAR
401 KYNRNETYIR ENFLVLDVFF EALTSEAMEQ RAAYGLSALL GDLGGQMGLF
451 IGASILTLE ILDYIYEVSW DRLKRVWRRP KTPLRTSTGG ISTLGLQELK
501 EQSPCENRGR AEGGGASNLL PNHHHPHGPP GSLFENFAC

10 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 526 amino acids

(B) TYPE: Protein

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: ASIC protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 3:

1 MELKTEEEV GGVQPVSQA FASSSTLHGL AHFSYERLS LKRALWALCF
51 LGSLAVLLCV CTERVQYYFC YHHVTKLDEV AASQLTFPAV TLCNLNEFRF
101 SQVSKNDLYH AGELLALLNN RYEIPDTQMA DEKQLEILQD KANFRSFKPK
151 PFNMREFYDR AGHDIRDMLL SCHFRGEACS AEDFKVVFTY YGKCYTFNSG
201 QDGRPRLKTM KGGTGNGLI MLDIQQDEYL PVWGETDETS FEAGIKVQIH
251 SQDEPPFIDQ LGFGVAPGFQ TFVSCQEORL IYLPSPWGTC NAVTMDSDFF
301 DYSITACRI DCETRYLVEN CNCRMVHMPG DAPYCTPEQY KECADPALDF
351 LVEKDQEYCV CEMPCNLTRY GKELSMVKIP SKASAKYLAK KFNKSEQYIG

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401 ENILVLDIFF EVLNYETIEQ KKAYEIAGLL GDIGGQMGLF IGASILTVLE
451 LFDYAYEVIK HRLCRRGKCQ KEAKRSSADK GVALSLDDVK RHNPCESLRG
501 HPAGMTYAAN ILPHHPARGT FEDFTC

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: Neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAGCAGTGAGGCTCTGGCCAGTCCCA

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: Dorsal root ganglion

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGACCTTCTGTCCCAGGAATAGG

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: Dorsal root ganglion

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 GACCTGGCTACCTTTGCCAGCACCA

(2) INFORMATION FOR SEQ ID NO: 7:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: neurons

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

8

ATATGGGTAGGTATTCTCTGCTG

2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

C/AGI,TAT/C,GG/CI,AAA/G,GAA/G,T/C/ATI,TCI,ATG

2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

IC/TT/A,IGC,ICC,IAT,A/GAA,IAG/A,ICC